<u>Amendments to the Claims</u>:

This listing of claims will replace all prior versions, and listings, of claims in the application:

<u>Listing of Claims</u>:

1. – 4. (Canceled)

5.   (Currently Amendeds) A method of differentiating between attenuated and virulent strains of PRRSV, said strains having RNA which is cleaved into known fragment numbers or lengths after cleavage by ~~a~~ <u>the Nsp1</u> restriction enzyme, depending upon whether the strain is attenuated or virulent, said method comprising the steps of:

obtaining a sample containing PRRSV viral RNA;

isolating said RNA from said sample;

digesting said RNA with said restriction enzyme;

determining fragment numbers or lengths after said digesting; ~~and~~

correlating said determined fragment numbers or lengths with said known fragment

numbers or lengths<u>; and</u>

<u>differentiating between attenuated and virulent strains of PRRSV based on the results</u>

<u>of said correlating step</u>.

6.   (Canceled)

7.   (Original) The method of claim 5, said known fragment lengths including fragments of about 476, 380, and 173 base pairs in length.

8.   (Canceled)

9.   (Original) The method of claim 8, said isolated RNA including a portion approximately 1 Kb in length.

10.   (Original) The method of claim 9, said 1 Kb portion being subjected to said digesting.

11.   (Original) The method of claim 9, further including the step of performing RT-PCR on said 1 Kb portion.

12. – 19. (Canceled)

20.   (New) A method of predicting whether a PRRSV strain will be virulent or avirluent comprising the steps of:

      digesting isolated PRRSV RNA with the Nsp1 restriction enzyme;

      determining the number of fragments resulting from said digesting step; and

      basing the prediction on the number of said resultant fragments, wherein a prediction

         of virulence will result when the digestion results in two or fewer fragments.

21.   (New) A method of predicting whether a PRRSV strain will be virulent

comprising the steps of:

counting the number of Nsp1 restriction sites in a PRRSV RNA sequence; and

predicting that the strain will be virulent when there is one or zero Nsp1 restriction

sites in said sequence.